

re-run



IFWO

RAW SEQUENCE LISTING

DATE: 10/15/2004

PATENT APPLICATION: US/10/645,012

TIME: 10:22:28

Input Set : N:\Crif3\RULE60\10645012.RAW.txt

Output Set: N:\CRF4\10152004\J645012.raw

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1 <110> APPLICANT: Tsuchiya, Masayuki
2   Saito, Mikiyoshi
3   Ohtomo, Toshihiko
4 <120> TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
5 <130> FILE REFERENCE: 06501-070001
6 <140> CURRENT APPLICATION NUMBER: 10/645,012
7 <141> CURRENT FILING DATE: 2003-08-21
8 <150> PRIOR APPLICATION NUMBER: US/09/700,820
9 <151> PRIOR FILING DATE: 2000-11-20
10 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02341
11 <151> PRIOR FILING DATE: 1999-04-30
12 <150> PRIOR APPLICATION NUMBER: JP 10/138652
13 <151> PRIOR FILING DATE: 1998-05-20
14 <150> PRIOR APPLICATION NUMBER: JP 10/279876
15 <151> PRIOR FILING DATE: 1998-10-01
16 <160> NUMBER OF SEQ ID NOS: 39
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 15
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Description of Artificial Sequence:Peptide Linker Sequence
23 <400> SEQUENCE: 1
24   Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
25   1           5           10           15
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 1035
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1035)
33 <400> SEQUENCE: 2
34   atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg      48
35   Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Pro
36   1           5           10           15
37   gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga      96
38   Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
39   20           25           30
40   ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg      144
41   Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
42   35           40           45
43   ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag      192

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46	Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys	
47	50 55 60	
48	ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg	240
49	Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg	
50	65 70 75 80	
51	ctg ctg ctg agg tgc gtg cag ctc cac gac tct gga aac tat tca tgc	288
52	Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys	
53	85 90 95	
54	tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt	336
55	Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val	
56	100 105 110	
57	ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc	384
58	Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser	
59	115 120 125	
60	aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca	432
61	Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr	
62	130 135 140	
63	aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac	480
64	Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp	
65	145 150 155 160	
66	ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc	528
67	Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys	
68	165 170 175	
69	cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg	576
70	Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met	
71	180 185 190	
72	tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt	624
73	Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe	
74	195 200 205	
75	cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc	672
76	Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val	
77	210 215 220	
78	act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac	720
79	Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp	
80	225 230 235 240	
81	ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga	768
82	Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg	
83	245 250 255	
84	tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac	816
85	Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp	
86	260 265 270	
87	ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac	864
88	Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His	
89	275 280 285	
90	gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc	912
91	Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser	
92	290 295 300	
93	gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt	960
94	Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser	

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95      305      310      315      320
96      cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act      1008
97      Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
98      325      330      335
99      aat aaa gac gat gat aat att ctc ttc      1035
100     Asn Lys Asp Asp Asp Asn Ile Leu Phe
101     340      345
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 40
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R1", an artificially
synthesized primer sequence
109 <400> SEQUENCE: 3
110     ttcgaattcc caccatgctg gccgtcggct gcgcgctgct      40
112 <210> SEQ ID NO: 4
113 <211> LENGTH: 36
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R2", an artificially
synthesized primer sequence
118 <400> SEQUENCE: 4
119     ttcgaattcg aagagaatat tatcatcgtc tttatt      36
121 <210> SEQ ID NO: 5
122 <211> LENGTH: 768
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (1)..(768)
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: a designed single chain
Fv gene sequence
130 <400> SEQUENCE: 5
131     cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag      48
132     Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
133     1      5      10      15
134     acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat      96
135     Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
136     20      25      30
137     cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg      144
138     His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
139     35      40      45
140     att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc      192
141     Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
142     50      55      60
143     aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc      240
144     Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
145     65      70      75      80
146     ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt      288

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147	Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
148		85 90 95
149	gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc	336
150	Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly	
151		100 105 110
152	agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt ggt ggt ggt	384
153	Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
154		115 120 125
155	tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc cca agc agc	432
156	Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
157		130 135 140
158	ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc	480
159	Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
160		145 150 155 160
161	cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag	528
162	Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
163		165 170 175
164	gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg	576
165	Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
166		180 185 190
167	cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc	624
168	Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
169		195 200 205
170	atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag	672
171	Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
172		210 215 220
173	ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc	720
174	Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
175		225 230 235 240
176	aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat	768
177	Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
178		245 250 255
180	<210> SEQ ID NO: 6	
181	<211> LENGTH: 32	
182	<212> TYPE: DNA	
183	<213> ORGANISM: Artificial Sequence	
184	<220> FEATURE:	
185	<223> OTHER INFORMATION: Description of Artificial Sequence: "TMT1", an artificially synthesized primer sequence	
186	<400> SEQUENCE: 6	
187	ggtgtcgact cccaggtcca actgcaggag ag	32
189	<210> SEQ ID NO: 7	
190	<211> LENGTH: 32	
191	<212> TYPE: DNA	
192	<213> ORGANISM: Artificial Sequence	
193	<220> FEATURE:	
194	<223> OTHER INFORMATION: Description of Artificial Sequence: "LINK1", an artificially synthesized primer sequence	
195	<400> SEQUENCE: 7	
196	ctcgtcacag tctcctcagg tgggtggtggt tc	32
198	<210> SEQ ID NO: 8	

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199 <211> LENGTH: 38
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK3", an artificially
synthesized primer sequence
204 <400> SEQUENCE: 8
205     gacatccaga tgaccagag cccaagcagc ctgagcgc                      38
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 63
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: "SCP-C", an artificially
synthesized primer sequence
213 <400> SEQUENCE: 9
214     gctgaattct tattatttat cgtcatcgtc tttgtagtca agcttatcag atggcgggaa      60
215     gat                                                                63
217 <210> SEQ ID NO: 10
218 <211> LENGTH: 9
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
223 <400> SEQUENCE: 10
224     Met Asp Tyr Lys Asp Asp Asp Lys
225     1             5
227 <210> SEQ ID NO: 11
228 <211> LENGTH: 34
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK2", an artificially
synthesized primer sequence
233 <400> SEQUENCE: 11
234     aaccaccacc acctgaggag actgtgacga ggct                      34
236 <210> SEQ ID NO: 12
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK4", an artificially
synthesized primer sequence
242 <400> SEQUENCE: 12
243     aggctgcttg ggctctgggt catctggatg tccga                      35
245 <210> SEQ ID NO: 13
246 <211> LENGTH: 36
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: "TMT2", an artificially
synthesized primer sequence
251 <400> SEQUENCE: 13

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252 atccgcggcc gcttattatt tatcgtcac gtcttt

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/645,012

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Input Set : N:\Crf3\RULE60\10645012.RAW.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23
Seq#:3; Line(s) 108
Seq#:4; Line(s) 117
Seq#:5; Line(s) 129
Seq#:6; Line(s) 185
Seq#:7; Line(s) 194
Seq#:8; Line(s) 203
Seq#:9; Line(s) 212
Seq#:11; Line(s) 232
Seq#:12; Line(s) 241
Seq#:13; Line(s) 250
Seq#:15; Line(s) 270
Seq#:16; Line(s) 280
Seq#:18; Line(s) 477
Seq#:19; Line(s) 486
Seq#:20; Line(s) 495
Seq#:21; Line(s) 507
Seq#:22; Line(s) 620
Seq#:23; Line(s) 633
Seq#:26; Line(s) 758
Seq#:27; Line(s) 838
Seq#:28; Line(s) 918
Seq#:29; Line(s) 927
Seq#:30; Line(s) 940
Seq#:31; Line(s) 1047
Seq#:32; Line(s) 1056
Seq#:33; Line(s) 1065
Seq#:34; Line(s) 1077
Seq#:35; Line(s) 1205
Seq#:36; Line(s) 1214
Seq#:37; Line(s) 1224
Seq#:38; Line(s) 1233
Seq#:39; Line(s) 1245

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/645,012

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Input Set : N:\Crf3\RULE60\10645012.RAW.txt

Output Set: N:\CRF4\10152004\J645012.raw

L:295 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 17, CDS LOCATION:29..2839